

IN THE CLAIMS:

Please amend the claims as follows:

1. (Amended) An isolated nucleic acid molecule from *Magnaporthe grisea* comprising a segment of chromosome 1 approximately 1 kb in size and containing at least one open reading frame, the segment conferring rice cultivar CO39-specific avirulence to fungal plant pathogens that contain the nucleic acid.

2. (Amended) The nucleic acid molecule of claim 1, having a nucleotide sequence at least 60 % identical to SEQ ID NO:1, the identity being calculated by hybridization with SEQ ID NO:1 under conditions derived from a formula of:

$$T_m = 81.5^{\circ}\text{C} + 16.6\text{Log} + 0.41(\% \text{ G+C}) - 0.63 (\% \text{ formamide}) - 600/\text{\#bp in duplex.}$$

4. (Amended) The nucleic acid molecule of claim 1, which encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

7. (Amended) A non-mammalian cell transformed with the recombinant DNA molecule of claim 6.

8. (Amended) The cell of claim 7, wherein said cell is either bacterial, fungal, insect, or plant.

9. (Amended) The cell of claim 8, which is an epiphytic bacterial cell.

10. (Amended) A transgenic plant regenerated from the cell of claim 8.

11. (Amended) An isolated nucleic acid molecule comprising a sequence selected from the group consisting of:

- a) SEQ ID NO:1;
- b) an allelic variant of an isolated nucleic acid molecule comprising SEQ ID NO:1;
- c) a segment of SEQ ID NO: 1 selected from the group consisting of:
  - an open reading frame located between nucleotides 358 and 495;
  - an open reading frame located between nucleotides 443 and 676;
  - an open reading frame located between nucleotides 582 and 850;
  - an open reading frame located between nucleotides 753 and 858;
  - an open reading frame located between nucleotides 885 and 1047;
  - an open reading frame on the complementary strand of SEQ ID NO:1 located between nucleotides 757 and 561;
  - an open reading frame on the complementary strand of SEQ ID NO: 1 located between nucleotides 419 and 312;
- d) an allelic variant of the segment of SEQ ID NO:1;
- e) a sequence that hybridizes with any of the sequences of a) - d) or its complement under high stringency conditions; and
- f) a sequence encoding a polypeptide having an amino acid sequence comprising any one of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

14. (Amended) A non-mammalian cell transformed with the recombinant DNA molecule of claim 13.

25. (Amended) A transgenic epiphytic bacterium that expresses a portion of an AVR1-CO39 gene which confers rice cultivar CO39-specific avirulence to microorganisms expressing the gene.

26. (Amended) The transgenic epiphytic bacterium of claim 25, which expresses the amino acid sequence of SEQ ID NO:4, or an allelic variant thereof.